SEQUENCE LISTING

<110> Burns, Jennifer M.
Summers, Bretton
Howard, Maureen C.
Schall, Thomas J.
ChemoCentryx, Inc.

<120> Compositions and Methods for Detecting and Treating
Diseases and Conditions Related to Chemokine Receptors

<130> 019934-003360US

<140> US 10/698,541
<141> 2003-10-30

<150> US 60/337,961
<151> 2001-11-30

<150> US 60/338,100
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<151> 2002-09-16

<150> US 60/434,912
<151> 2002-12-20

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<151> 2003-05-30

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<170> PatentIn Ver. 2.1

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<220>
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coding sequence

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<213> Homo sapiens

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Ile Ser Trp Pro Cys Asn Ser Ser Asp Cys Ile Val Val Asp Thr Val
             20                  25                  30

Met Cys Pro Asn Met Pro Asn Lys Ser Val Leu Leu Tyr Thr Leu Ser
         35                  40                  45

Phe Ile Tyr Ile Phe Ile Phe Val Ile Gly Met Ile Ala Asn Ser Val
     50                  55                  60

Val Val Trp Val Asn Ile Gln Ala Lys Thr Thr Gly Tyr Asp Thr His
 65                  70                  75                  80

Cys Tyr Ile Leu Asn Leu Ala Ile Ala Asp Leu Trp Val Val Leu Thr
                 85                  90                  95

Ile Pro Val Trp Val Val Ser Leu Val Gln His Asn Gln Trp Pro Met
            100                 105                 110

Gly Glu Leu Thr Cys Lys Val Thr His Leu Ile Phe Ser Ile Asn Leu
        115                 120                 125

Phe Gly Ser Ile Phe Phe Leu Thr Cys Met Ser Val Asp Arg Tyr Leu
    130                 135                 140

Ser Ile Thr Tyr Phe Thr Asn Thr Pro Ser Ser Arg Lys Lys Met Val
145                 150                 155                 160

Arg Arg Val Val Cys Ile Leu Val Trp Leu Leu Ala Phe Cys Val Ser
                165                 170                 175

Leu Pro Asp Thr Tyr Tyr Leu Lys Thr Val Thr Ser Ala Ser Asn Asn
            180                 185                 190

Glu Thr Tyr Cys Arg Ser Phe Tyr Pro Glu His Ser Ile Lys Glu Trp
        195                 200                 205

Leu Ile Gly Met Glu Leu Val Ser Val Val Leu Gly Phe Ala Val Pro
    210                 215                 220

Phe Ser Ile Ile Ala Val Phe Tyr Phe Leu Leu Ala Arg Ala Ile Ser
225                 230                 235                 240

Ala Ser Ser Asp Gln Glu Lys His Ser Ser Arg Lys Ile Ile Phe Ser
                245                 250                 255
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Tyr Val Val Val Phe Leu Val Cys Trp Leu Pro Tyr His Val Ala Val
            260                 265                 270

Leu Leu Asp Ile Phe Ser Ile Leu His Tyr Ile Pro Phe Thr Cys Arg
        275                 280                 285

Leu Glu His Ala Leu Phe Thr Ala Leu His Val Thr Gln Cys Leu Ser
    290                 295                 300

Leu Val His Cys Cys Val Asn Pro Val Leu Tyr Ser Phe Ile Asn Arg
305                 310                 315                 320

Asn Tyr Arg Tyr Glu Leu Met Lys Ala Phe Ile Phe Lys Tyr Ser Ala
                325                 330                 335

Lys Thr Gly Leu Thr Lys Leu Ile Asp Ala Ser Arg Val Ser Glu Thr
            340                 345                 350

Glu Tyr Ser Ala Leu Glu Gln Ser Thr Lys
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<210> 3
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<212> DNA
<213> Homo sapiens

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<223> G-protein coupled receptor (GPCR) CCX-CKR2.2
coding sequence

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agcgtcctgc tctacacgct ctccttcatt tacattttca tcttcgtcat cggcatgatt 180
gccaactccg tggtggtctg ggtgaatatc caggccaaga ccacaggcta tgacacgcac 240
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gaccgctacc tctccatcac ctacttcacc aacaccccca gcagcaggaa gaagatggta 480
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cccgagcaca gcatcaagga gtggctgatc ggcatggagc tggtctccgt tgtcttgggc 660
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gcgtccagtg accaggagaa gcacagcagc cggaagatca tcttctccta cgtggtggtc 780
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<210> 4
<211> 362
<212> PRT
<213> Homo sapiens

<220>
<223> G-protein coupled receptor (GPCR) CCX-CKR2.2

<400> 4

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 1               5                  10                  15

Ile Ser Trp Pro Cys Asn Ser Ser Asp Cys Ile Val Val Asp Thr Val
            20                  25                  30

Met Cys Pro Asn Met Pro Asn Lys Ser Val Leu Leu Tyr Thr Leu Ser
        35                  40                  45

Phe Ile Tyr Ile Phe Ile Phe Val Ile Gly Met Ile Ala Asn Ser Val
    50                  55                  60

Val Val Trp Val Asn Ile Gln Ala Lys Thr Thr Gly Tyr Asp Thr His
65                  70                  75                  80

Cys Tyr Ile Leu Asn Leu Ala Ile Ala Asp Leu Trp Val Val Leu Thr
                85                  90                  95

Ile Pro Val Trp Val Val Ser Leu Val Gln His Asn Gln Trp Pro Met
            100                 105                 110

Gly Glu Leu Thr Cys Lys Val Thr His Leu Ile Phe Ser Ile Asn Leu
        115                 120                 125

Phe Ser Gly Ile Phe Phe Leu Thr Cys Met Ser Val Asp Arg Tyr Leu
    130                 135                 140

Ser Ile Thr Tyr Phe Thr Asn Thr Pro Ser Ser Arg Lys Lys Met Val
145                 150                 155                 160

Arg Arg Val Val Cys Ile Leu Val Trp Leu Leu Ala Phe Cys Val Ser
                165                 170                 175

Leu Pro Asp Thr Tyr Tyr Leu Lys Thr Val Thr Ser Ala Ser Asn Asn
            180                 185                 190

Glu Thr Tyr Cys Arg Ser Phe Tyr Pro Glu His Ser Ile Lys Glu Trp
        195                 200                 205

Leu Ile Gly Met Glu Leu Val Ser Val Val Leu Gly Phe Ala Val Pro
    210                 215                 220

Phe Ser Ile Ile Ala Val Phe Tyr Phe Leu Leu Ala Arg Ala Ile Ser
225                 230                 235                 240

Ala Ser Ser Asp Gln Glu Lys His Ser Ser Arg Lys Ile Ile Phe Ser
                245                 250                 255

Tyr Val Val Val Phe Leu Val Cys Trp Leu Pro Tyr His Val Ala Val
            260                 265                 270

Leu Leu Asp Ile Phe Ser Ile Leu His Tyr Ile Pro Phe Thr Cys Arg
        275                 280                 285

Leu Glu His Ala Leu Phe Thr Ala Leu His Val Thr Gln Cys Leu Ser
    290                 295                 300

Leu Val His Cys Cys Val Asn Pro Val Leu Tyr Ser Phe Ile Asn Arg
305                 310                 315                 320
```

```
Asn Tyr Arg Tyr Glu Leu Met Lys Ala Phe Ile Phe Lys Tyr Ser Ala
                325                 330                 335

Lys Thr Gly Leu Thr Lys Leu Ile Asp Ala Ser Arg Val Ser Glu Thr
            340                 345                 350

Glu Tyr Ser Ala Leu Glu Gln Asn Ala Lys
        355                 360
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<210> 5
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<212> DNA
<213> Homo sapiens

<220>
<223> G-protein coupled receptor (GPCR) CCX-CKR2.3
coding sequence

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gccaactccg tggtggtctg ggtgaatatc caggccaaga ccacaggcta tgacacgcac 240
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<213> Homo sapiens

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<223> G-protein coupled receptor (GPCR) CCX-CKR2.3

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Ile Ser Trp Pro Cys Asn Ser Ser Asp Cys Ile Val Val Asp Thr Val
            20                  25                  30

Met Cys Pro Asn Met Pro Asn Lys Ser Val Leu Leu Tyr Thr Leu Ser
        35                  40                  45

Phe Ile Tyr Ile Phe Ile Phe Val Ile Gly Met Ile Ala Asn Ser Val
    50                  55                  60
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```
Val Val Trp Val Asn Ile Gln Ala Lys Thr Thr Gly Tyr Asp Thr His
 65                  70                  75                  80

Cys Tyr Ile Leu Asn Leu Ala Ile Ala Asp Leu Trp Val Val Leu Thr
                85                  90                  95

Ile Pro Val Trp Val Val Ser Leu Val Gln His Asn Gln Trp Pro Met
            100                 105                 110

Gly Glu Leu Thr Cys Lys Val Thr His Leu Ile Phe Ser Ile Asn Leu
        115                 120                 125

Phe Gly Ser Ile Phe Phe Leu Thr Cys Met Ser Val Asp Arg Tyr Leu
    130                 135                 140

Ser Ile Thr Tyr Phe Thr Asn Thr Pro Ser Ser Arg Lys Lys Met Val
145                 150                 155                 160

Arg Arg Val Val Cys Ile Leu Val Trp Leu Leu Ala Phe Cys Val Ser
                165                 170                 175

Leu Pro Asp Thr Tyr Tyr Leu Lys Thr Val Thr Ser Ala Ser Asn Asn
            180                 185                 190

Glu Thr Tyr Cys Arg Ser Phe Tyr Pro Glu His Ser Ile Lys Glu Trp
        195                 200                 205

Leu Ile Gly Met Glu Leu Val Ser Val Val Leu Gly Phe Ala Val Pro
    210                 215                 220

Phe Ser Ile Val Ala Val Phe Tyr Phe Leu Leu Ala Arg Ala Ile Ser
225                 230                 235                 240

Ala Ser Ser Asp Gln Glu Lys His Ser Ser Arg Lys Ile Ile Phe Ser
                245                 250                 255

Tyr Val Val Val Phe Leu Val Cys Trp Leu Pro Tyr His Val Ala Val
            260                 265                 270

Leu Leu Asp Ile Phe Ser Ile Leu His Tyr Ile Pro Phe Thr Cys Arg
        275                 280                 285

Leu Glu His Ala Leu Phe Thr Ala Leu His Val Thr Gln Cys Leu Ser
    290                 295                 300

Leu Val His Cys Cys Val Asn Pro Val Leu Tyr Ser Phe Ile Asn Arg
305                 310                 315                 320

Asn Tyr Arg Tyr Glu Leu Met Lys Ala Phe Ile Phe Lys Tyr Ser Ala
                325                 330                 335

Lys Thr Gly Leu Thr Lys Leu Ile Asp Ala Ser Arg Val Ser Glu Thr
            340                 345                 350

Glu Tyr Ser Ala Leu Glu Gln Ser Thr Lys
        355                 360
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<210> 7
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<212> DNA
<213> Homo sapiens

<220>
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coding sequence

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accaaatga 1089

<210> 8
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<212> PRT
<213> Homo sapiens

<220>
<223> G-protein coupled receptor (GPCR) CCX-CKR2.4

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20 25 30

Met Cys Pro Asn Met Pro Asn Lys Ser Val Leu Leu Tyr Thr Leu Ser
35 40 45

Phe Ile Tyr Ile Phe Ile Phe Val Ile Gly Met Ile Ala Asn Ser Val
50 55 60

Val Val Trp Val Asn Ile Gln Ala Lys Thr Thr Gly Tyr Asp Thr His
65 70 75 80

Cys Tyr Ile Leu Asn Leu Ala Ile Ala Asp Leu Trp Val Val Leu Thr
85 90 95

Ile Pro Val Trp Val Val Ser Leu Val Gln His Asn Gln Trp Pro Met
100 105 110

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Gly Glu Leu Thr Cys Lys Val Thr His Leu Ile Phe Ser Ile Asn Leu
        115                 120                 125

Phe Gly Ser Ile Phe Phe Leu Thr Cys Met Ser Val Asp Arg Tyr Leu
    130                 135                 140

Ser Ile Thr Tyr Phe Thr Asn Thr Pro Ser Ser Arg Lys Lys Met Val
145                 150                 155                 160

Arg Arg Val Val Cys Ile Leu Val Trp Leu Leu Ala Phe Cys Val Ser
                165                 170                 175

Leu Pro Asp Thr Tyr Tyr Leu Lys Thr Val Thr Ser Ala Ser Asn Asn
            180                 185                 190

Glu Thr Tyr Cys Arg Ser Phe Tyr Pro Glu His Ser Ile Lys Glu Trp
        195                 200                 205

Leu Ile Gly Met Glu Leu Val Ser Val Val Leu Gly Phe Ala Val Pro
    210                 215                 220

Phe Ser Ile Ile Ala Val Phe Tyr Phe Leu Leu Ala Arg Ala Ile Ser
225                 230                 235                 240

Ala Ser Ser Asp Gln Glu Lys His Ser Ser Arg Lys Ile Ile Phe Ser
                245                 250                 255

Tyr Val Val Val Phe Leu Val Cys Trp Leu Pro Tyr His Val Ala Val
            260                 265                 270

Leu Leu Asp Ile Phe Ser Ile Leu His Tyr Ile Pro Phe Thr Cys Arg
        275                 280                 285

Leu Glu His Ala Leu Phe Thr Ala Leu His Val Thr Gln Cys Leu Ser
    290                 295                 300

Leu Val His Cys Cys Val Asn Pro Val Leu Tyr Ser Phe Ile Asn Arg
305                 310                 315                 320

Asn Tyr Arg Tyr Glu Leu Met Lys Ala Phe Ile Phe Lys Tyr Ser Ala
                325                 330                 335

Lys Thr Gly Leu Thr Lys Leu Ile Asp Ala Ser Arg Val Ser Glu Thr
            340                 345                 350

Glu Tyr Ser Ala Leu Glu Gln Ser Thr Lys
        355                 360
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<212> DNA
<213> Homo sapiens

<220>
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accaaatga                                                        1089
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<210> 10
<211> 362
<212> PRT
<213> Homo sapiens

<220>
<223> G-protein coupled receptor (GPCR) CCX-CKR2.5

<400> 10

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  1               5                  10                  15

Ile Ser Trp Pro Cys Asn Ser Ser Asp Cys Ile Val Val Asp Thr Val
             20                  25                  30

Met Cys Pro Asn Met Pro Asn Lys Ser Val Leu Leu Tyr Thr Leu Ser
         35                  40                  45

Phe Ile Tyr Ile Phe Ile Phe Val Ile Gly Met Ile Ala Asn Ser Val
     50                  55                  60

Val Val Trp Val Asn Ile Gln Ala Lys Thr Thr Gly Tyr Asp Thr His
 65                  70                  75                  80

Cys Tyr Ile Leu Asn Leu Ala Ile Ala Asp Leu Trp Val Val Leu Thr
                 85                  90                  95

Ile Pro Val Trp Val Val Ser Leu Val Gln His Asn Gln Trp Pro Met
            100                 105                 110

Gly Glu Leu Thr Cys Lys Val Thr His Leu Ile Phe Ser Ile Asn Leu
        115                 120                 125

Phe Ser Ser Ile Phe Phe Leu Thr Cys Met Ser Val Asp Arg Tyr Leu
    130                 135                 140

Ser Ile Thr Tyr Phe Thr Asn Thr Pro Ser Ser Arg Lys Lys Met Val
145                 150                 155                 160

Arg Arg Val Val Cys Ile Leu Val Trp Leu Leu Ala Phe Cys Val Ser
                165                 170                 175
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Leu Pro Asp Thr Tyr Tyr Leu Lys Thr Val Thr Ser Ala Ser Asn Asn
            180                 185                 190

Glu Thr Tyr Cys Arg Ser Phe Tyr Pro Glu His Ser Ile Lys Glu Trp
        195                 200                 205

Leu Ile Gly Met Glu Leu Val Ser Val Val Leu Gly Phe Ala Val Pro
    210                 215                 220

Phe Ser Ile Ile Ala Val Phe Tyr Phe Leu Leu Ala Arg Ala Ile Ser
225                 230                 235                 240

Ala Ser Ser Asp Gln Glu Lys His Ser Ser Arg Lys Ile Ile Phe Ser
                245                 250                 255

Tyr Val Val Val Phe Leu Val Cys Trp Leu Pro Tyr His Val Ala Val
            260                 265                 270

Leu Leu Asp Ile Phe Ser Ile Leu His Tyr Ile Pro Phe Thr Cys Arg
        275                 280                 285

Leu Glu His Ala Leu Phe Thr Ala Leu His Val Thr Gln Cys Leu Ser
    290                 295                 300

Leu Val His Cys Cys Val Asn Pro Val Leu Tyr Ser Phe Ile Asn Arg
305                 310                 315                 320

Asn Tyr Arg Tyr Glu Leu Met Lys Ala Phe Ile Phe Lys Tyr Ser Ala
                325                 330                 335

Lys Thr Gly Leu Thr Lys Leu Ile Asp Ala Ser Arg Val Ser Glu Thr
            340                 345                 350

Glu Tyr Ser Ala Leu Glu Gln Ser Thr Lys
        355                 360
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